SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Method of stabilizing protein solutions

<130> C1-A0319P

<150> JP 2003-351410
<151> 2003-10-09

<160> 18

<170> PatentIn version 3.1

<210> 1
<211> 1779
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (1)..(1779)
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<400> 1

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atg gag ttt ggg ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt      48
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1               5                   10                  15


gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag      96
Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
                20                  25                  30


cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt     144
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            35                  40                  45
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agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg   192
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
   50   55   60

gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca   240
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
   65   70   75   80

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac   288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
          85   90   95

acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta   336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
          100   105   110

tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct   384
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
          115   120   125

tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc   432
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
   130   135   140

cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcg gat acg   480
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
145   150   155   160

agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt ccc gac tcc   528
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
          165   170   175

atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc   576
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
          180   185   190

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cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca     624
Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
         195                 200             205


cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gaa cac     672
Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
     210                 215             220


gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg     720
Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
225                 230             235                 240


cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc     768
Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
             245             250             255


cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc     816
Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
             260                 265             270


tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg     864
Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
         275                 280             285


cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag     912
Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
     290                 295             300


gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca     960
Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
305                 310             315                 320


ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc     1008
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
             325                 330             335


cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg     1056
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Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
        340   345   350

tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca   1104
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
        355   360   365

tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg   1152
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
        370   375   380

gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc   1200
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
385   390   395   400

cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac   1248
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
           405   410   415

ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat   1296
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
          420   425   430

gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac   1344
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
        435   440   445

ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc   1392
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
        450   455   460

ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg   1440
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
465   470   475   480

aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct   1488
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser

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                    485                  490                  495

ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc        1536
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
              500                  505                  510


ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca        1584
Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
              515                  520                  525


ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg        1632
Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
          530                  535                  540


aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc        1680
Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
545                  550                  555                  560


aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc        1728
Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
                  565                  570                  575


ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac        1776
Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
              580                  585                  590


tga                                                                     1779
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<210> 2
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<212> PRT
<213> Homo sapiens

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1               5                   10                  15
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Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
            20   25   30

Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            35   40   45

Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        50   55   60

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
65   70   75   80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
                85   90   95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100   105   110

Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
            115   120   125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
            130   135   140

Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
145   150   155   160

Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
                165   170   175

Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
                180   185   190

Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
            195   200   205

Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
            210   215   220

Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
225   230   235   240

Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
                245   250   255

Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
            260   265   270

Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
            275   280   285

Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
            290   295   300

Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr

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        305                    310.                   315                   320
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
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Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
                     340                   345                  ·350
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
             355                   360                   365
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
             370                   375                   380
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
385                   390                   395                   400
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
                     405                   410                   415
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
                     420                   425                   430
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
             435                  .440                   445
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
             450                   455                   460
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
465                   470                   475                   480
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
                     485                   490                   495
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser.
                     500                   505                   510
Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
             515                   520                   525
Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
             530                   535                   540
Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
545                   550                   555                   560
Asn Arg Val Thr Glu Arg Thr Val Asp Lys·Ser Thr Gly Lys Pro Thr
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             580                   585                   590
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<210> 3

<211> 723

<212> DNA

<213> Homo sapiens

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<222> (1)..(723)

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15


ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct        96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
                20                  25                  30


gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt       144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
            35                  40                  45


gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag       192
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
        50                  55                  60


aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg       240
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65                  70                  75                  80


gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat       288
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95


ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat       336
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
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                    100                105                110

tac tgt cag caa tat tat agt act cct ccg acg ttc ggc caa ggg acc        384
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
        115                120                125


aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc        432
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
        130                135                140


ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc        480
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
145                150                155                160


ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg        528
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
                165                170                175


gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag        576
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
                180                185                190


gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc        624
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
        195                200                205


aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat        672
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
        210                215                220


cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt        720
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                230                235                240


tag                                                                    723
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<210> 4
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<212> PRT
<213> Homo sapiens

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            20   25   30
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
        35   40   45
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
    50   55   60
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65   70   75   80
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85   90   95
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
                100   105   110
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
            115   120   125
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
        130   135   140
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
145   150   155   160
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
                165   170   175
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
            180   185   190
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
            195   200   205
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
        210   215   220
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225   230   235   240

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<212> DNA
<213> Homo sapiens

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Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys
1               5                   10                  15


gct gtt cat gtg aaa gcc caa gaa gat gaa agg att gtt ctt gtt gac      96
Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp
                20                  25                  30


aac aaa tgt aag tgt gcc cgg att act tcc agg atc atc cgt tct tcc     144
Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
            35                  40                  45


gaa gat cct aat gag gac att gtg gag aga aac atc cga att att gtt     192
Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val
        50                  55                  60


cct ctg aac aac agg gag aat atc tct gat ccc acc tca cca ttg aga     240
Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
65                  70                  75                  80


acc aga ttt gtg tac cat ttg tct gac ctc tgt aaa aaa tgt gat cct     288
Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro
                85                  90                  95


aca gaa gtg gag ctg gat aat cag ata gtt act gct acc cag agc aat     336
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Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn
          100   105   110

atc tgt gat gaa gac agt gct aca gag acc tgc tac act tat gac aga   384
Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg
        115   120   125

aac aag tgc tac aca gct gtg gtc cca ctc gta tat ggt ggt gag acc   432
Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr
    130   135   140

aaa atg gtg gaa aca gcc tta acc cca gat gcc tgc tat cct gac taa   480
Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
145   150   155

<210> 6
<211> 159
<212> PRT
<213> Homo sapiens

<400> 6
Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys
1   5   10   15
Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp
        20   25   30
Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
      35   40   45
Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val
    50   55   60
Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
65   70   75   80
Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro
        85   90   95
Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn
        100   105   110
Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg

```
                115                   120                  125
Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr
         130                   135                  140
Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
145                    150                   155
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<210> 7
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<213> Artificial

<220>
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<210> 8
<211> 24
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized sequence

<400> 8
aacatgctct ggccgagcca gtcg   24

<210> 9
<211> 24
<212> DNA
<213> Artificial

<220>

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<400> 9
gcaagtccag ccagagtgtt ttat 24

<210> 10
<211> 24
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized sequence

<400> 10
ctgtccttgc tgtcctgctc tgtg 24

<210> 11
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<212> DNA
<213> Artificial

<220>
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<210> 12
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<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

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<210> 13
<211> 32
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 13
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<210> 14
<211> 30
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 14
ggagcaggcg gccgcacttc tccctctaac   30

<210> 15
<211> 24
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized sequence

<400> 15
accattgaga accagatttg tgta   24

<210> 16
<211> 24
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized sequence

<400> 16
tgtgtagcac ttgtttctgt cata   24

<210> 17
<211> 28
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 17
atgaattcca ccatgaagaa ccatttgc   28

<210> 18
<211> 26
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 18

tatctagatt agtcaggata gcaggc   26